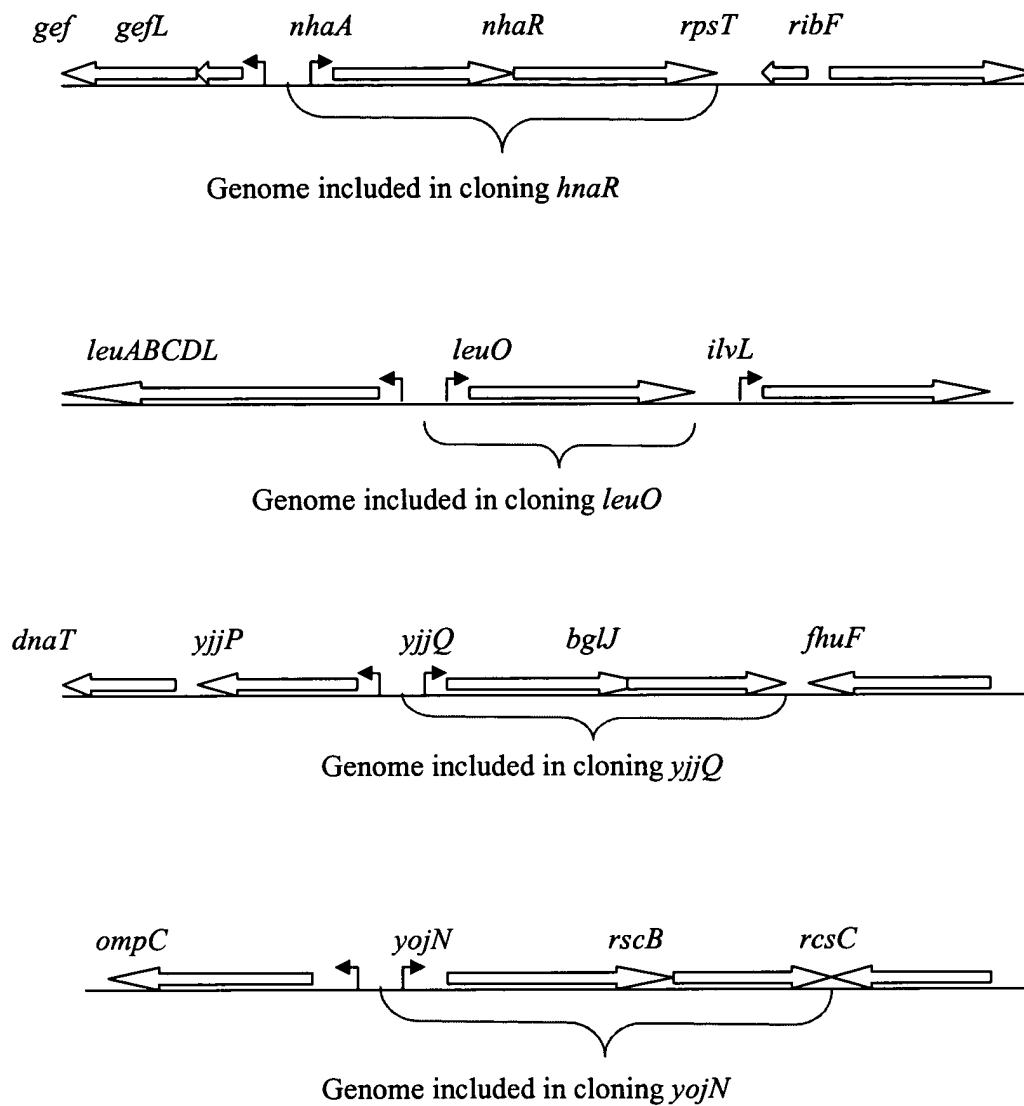


**Figure 1**



**Figure 2**

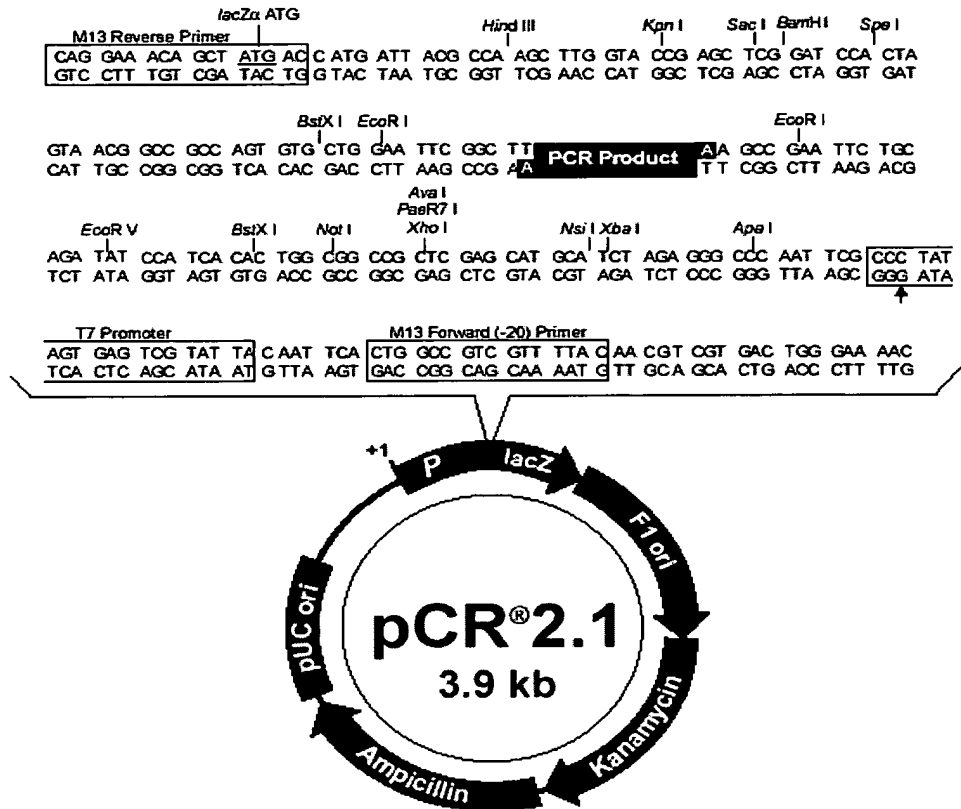
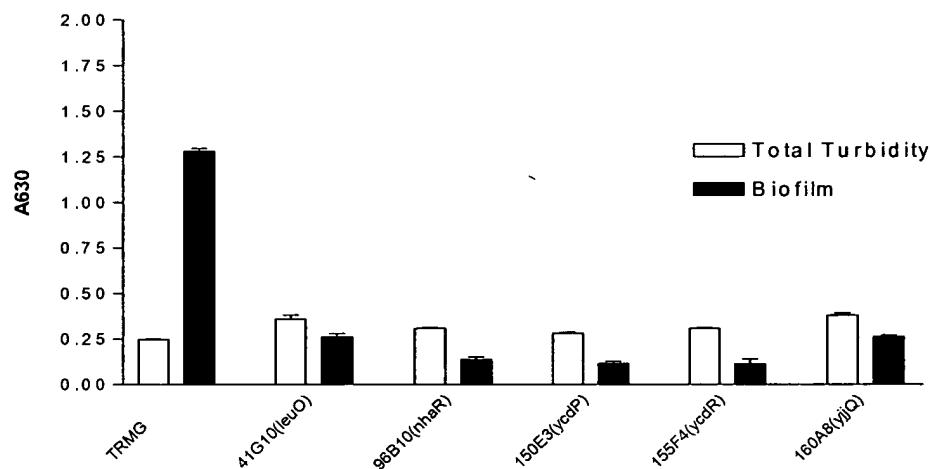
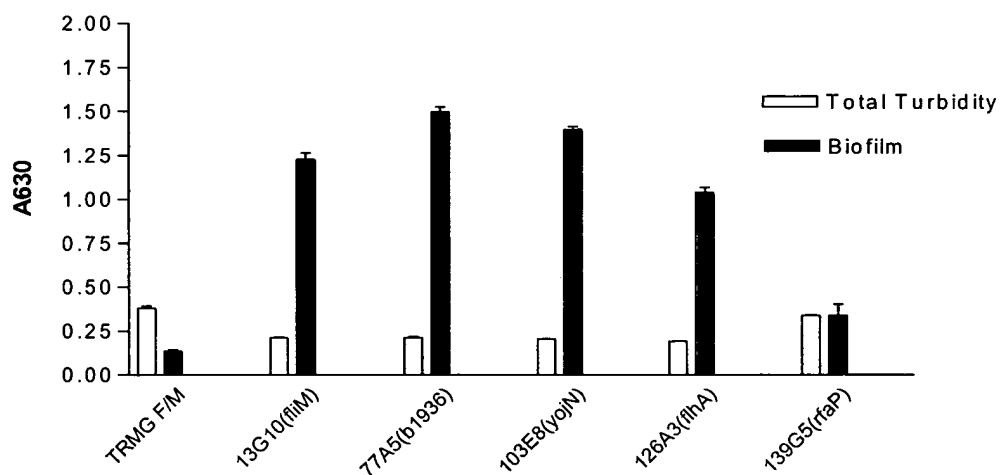


Figure 3



**Figure 4A**



**Figure 4b**



## Figure 5-4

### 14C10-4 (10X)

flgE gene – structural component; surface structures/ flagellar biosynthesis, hook protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74160

AACGGNCCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGATCANCCTGAATTCCAGTGATCCGCTTCCTACTGTTACGCCATTCCANNGCCNGCAATGCGGNTANCTNTN  
ACAAANAAGGTTNNGTGACTGTTTTCCACAGTCATGGTAATGCTCATGACATGAGCGTCTACTTTGTGNACC  
CGGGGATAATAACTGGCAGGTCTACACCCAGGATAGCAGTGATCCAAACAGCATTGCGAAGACAGCG

## Figure 5-5

### 36E2-5 (3X)

yhjH gene (complement) - orf; unknown function ; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_004431

Protein Accession # NP\_417982

AAACGGTTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TGCTTACACCTGGCAGCCGATCTATCAAAATGCGGGCGGTTAATGGCCGTGGAGCTATTAACGGT  
GGTCACGCATCCCTTGAACCTTCGCAACGCCTGCCGCCGGATCGCTATTTTACTGAAATCACCGT  
CAGCCATCGGATGGAGGTTGTGAAAGAGCAGATTGATTTGCTGGCGCAAAAAGCCGACTTCTTTAT  
AGAGCACGGCCTGCTGGCATCGGTCAATAT

## Figure 5-6

### 38G7-2 (11X)

fliM gene - Structural component; surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

AAACGGTTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTCCGGTATGGGTAAACTCGCGACCTT  
CCACTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTC  
GGTGAGAACACCACAGCCAGTGC CGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGG  
CACCGGCAGGTTGCGGGCAAATTCATGGTACGGCTGAATGCGGATGGCCCCGACGGTTATATCCN  
GNCNNNNNGTACTAGTCGACG

## Figure 5-7

### 39C9-2 (3X)

rep gene - enzyme; DNA replication, repair restriction/modification; product - rep helicase, a single-stranded DNA dependent ATPase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000454

Protein Accession # AAC76783

```
AAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATT  
CATCAG  
TATCCAGCCCCAACGTATGGAAAGTGGAGATCATCAGCCACGCGCCTCTTTGCGCCCCAGCGTCT  
GCCCTACACGCTCTTTCATCTCGCGCGCTGCTTTATTAGTAAAGGTCACCGCCGCAATGTGCCGCG  
CCTGATAACCGCAACCGCGGATCAGATGGGCGATTTTATTGGTGATAACACGAGTTTACCAGGAAC  
CCGCGCCCGCCAGCACCAGGCAGGGGCCGGTAACGAATTCGACAGCTTGTGTTGGCCGGGGTTT  
AGACGCATAGGTGTATTGCTCA
```

## Figure 5-8

### 42G6-4 (12X)

fliP gene – putative structure; surface structures/ flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
CGGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
TGGTACGCATCTACATAAATTTTGTTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGC  
CAGCCCCAGCAATACCTGGTTAGGTGGCGCGCGGAGGGTGTTCACGCGCGTTACGCAATAAACC  
AAAAACAATGATGATGCGGGTGAACTGGTCATCATCAGTAAAATTGCCGGAATAAACGTCAACG  
AGGTGATGAACACCAGCGTCTGCACCGGGAGC
```

## Figure 5-9

### 43B10-3 (11X)

fliG gene – Structural component; surface structure, flagella motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

```
NNCNNAACANACGGNCCGGCCNG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
CGGCGAGCTGGCGCAGAAAATCATCGACGAGATGTTCCCTGTTTCGAGAATCTGGTGGATNTCGCCAATCGCN  
GTACTAGTCGACGNGTGGCCAAANTGGATTCCNAATCGCTGNTGATCGCGCTGAAAGGAGCCGAGCNGTC  
ACTGTGCNAGAANTTCTTGCCNATATGTGCGCNCNATATCCCNCCNACCGTACCCCTNGN  
ACGNNNNACCGNACCCCNNTNCGNCAAGNATGNNANNANCCNGATANANCAAGNNCANTNCTNNGATN  
CACNNNATANNANNGNCGCCNAC
```

## Figure 5-10

### 43F5-2 (2.5X)

wecB gene - enzyme; Central intermediary metabolism; sugar-nucleotide synthesis, product - UDP -N-acetyl glucosamine-2-epimerase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000455

Protein Accession # AAC76791

```
AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGCATGCTCTCGCATTCTGGAAGCGTTAAAAAATAATCGGATATCACTATGAGTTTTGCGA
CCATTTCTGTTATCGGACTGGGTTATATCGGGCTGCCAACNGCTACNCGACNCGCCNCGGCAAA
AACAGGTAATTGGTGTGCATATCAACCAACATGCGGTTGATACCATCAATCGTGGCCAAATCCATA
TCCCCCCCCCGTACTAGTCGACG
```

## Figure 5-11

### 45C8-4 (4X)

frdA gene - enzyme; energy metabolism, carbon: anaerobic respiration; product is fumarate reductase, anaerobic flavoprotein subunit

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000487

Protein Accession # AAC77114

```
CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGCGCACGGCAAATCCGAATGCAAAAATCGCACTAATCTCAAAAAGTATACCCGATGCGTAGCCATACC
GTTGCTGCAGAAAGGGGGCTCCGCCGCTGTGCGCAGGATCATGACAGCTTCGAATATCCCCNNNCCCCCGT
ACTAGTCGACGCCGTGAANANNNN
```

## Figure 5-12

### 49G9-3 (12X)

fliP gene - putative structure; surface structures, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
AACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAG
ACTGGCGAATATCGGCCCGTTGCGTNCTACTCNACNCGTGCCNATGCGCATTTTGCTNCCNGCCTA
CGTGACCAGCGAGTTGAAAACCGCATTTTCAGATACGGCTTCACAGATTTTCATCCCTTTTTTGATTA
TCGACCTGGTGATAGCCAGCGTGTTGATGGC
```



## Figure 5-13

### 51B12-3 (6X)

fliM gene - flagella gene, flagella biosynthesis; motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
ATGAAAACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACTCAACTTCCAGCGGATTAATCGCCTTCCAGGCGTCGCTATAGCCTTCAAGCGCCAGTTTCAAC
ATGCGGTTGATGACGCGCTGTTCCGGTATGGGTAAACTCGCGACCTTCCACTTTGGTCGGGAAGCGT
CCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAGAA
```

## Figure 5-14

### 57E7-6 (7X)

fliP gene - flagella gene, putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCA
GACTGGCGAATACCGGCCCGTTGCAGGGACCTGAAGCCGTGCCGATGCGCATTTTGCTCCCGGCCT
ACGTGACCAGCGAGTTGAAAACCGCATTTTCAGATAGGCTTCACGATTTTCATCCCTTTTTTGATTAT
CGACCTGGTGATAGCCAGCGTGTTGATGGCATTGGGGATGATGATGGTT
```

## Figure 5-15

### 61G2-3 (10X)

255 bp down stream of flhB gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834

```
NGNNNATACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATTAAGCGTGAATGATGCCAGAGCGCAAAGCGTTCAATGGTTTGAGTAAGGGGCAAAACAGGCG
GGATTTAGGGCTTTTGCTGCCACATATCCNNNNNNNNNGTACTAGTCGACGCGTGGCCA
```

## Figure 5-16

### 63A9-1 (4X)

rfaQ gene (complement) – enzyme, macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_002695

Protein Accession # NP\_312534

```
AAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATGTGTACCGTGTATTGGCGCTAAGNGTGNGAAGCTTTTTTCCAANTACCATGCTTGCCNNATG
ACCATAANGTTGCGATATNTTCATTCCGTGCATGCAAACANCGTACCNNCAGCGCCACCATNCAAC
TGATGCGTCNGANTAATGACCAGGTTNTANTTATTCTNTCGCCCCGAGCCTCATCANCNAANGTCN
CTTTNTNNNCGGNANNNNNATTTTNCNCGTCTNNNTNTTGNNTNANTNNNTTACGCGGCNACNNA
TTNGTTNTGGTCNTACGNGCNNNATAACNGCNNCTCNCNNNCC
```

## Figure 5-17

### 64F2-1 (9X)

factor Sigma32 – promoter dnaKp2; documented +1 site at 12121

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D10765

Protein Accession # BAA01595

```
CGNCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGTTTCGCCCCCTATTACAGACTCACAACCACATGATGACCGAATATATAGTGGAGACGTTTAGATG
GGTAAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTGTAGCGATTATGGATGGCACCCT
CCTCGCGTGCTGGAGAACGCCGAAGGCGATCGCACCACGCCTTCTATCATTGCCTATACCCAGGAT
GGTGAACCTCTAGTTGGTCAGCCGGCTAAACGTCAGGCAGTGACGAACCCGCAAAACACTCTGTT
TGCGATTAAACGCCTGATTGGTCGCCGCTTCCAGGACGAAGAAGTACAGCGTGATGTTTCCATCAT
GCCGTTCAAATTATTGCTGCTGATATCCNCCCCCNG
```

## Figure 5-18

### 66F4-3 (10X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
TACCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTCCGGTATGGGTAAACTCGCGACCTT
CCACTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCGAGACTC
GGTGAGAACACCACAGCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTTCAGGTTGGTCGG
CACCGGCAGGTTGCGGGCAAATT
```

## Figure 5-19

### 67C8-4 (6X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NNCGTNCGG

GATATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG  
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTTCG  
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTTC  
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCATGATCGAGCCG  
CTACGGGAATTGTTGTTAACC CGCC

## Figure 5-20

### 67C9-6 (8X)

fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

ANCCGATCCGG

GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG  
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTTCG  
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTTC  
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATC

## Figure 5-21

### 67E10-5 (6.5X)

fliI gene - Enzyme, flagella synthesis; surface structures, flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

CGNCCGATCCGG

GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG  
CACCTTGCAATTCGACGAGCGGAGAAACATCCGCCGAGCGGCAATCACCACCTGAGCGTGCACGCCCTTCG  
GCACCGAGGATGTTCTCAATAAAATCTTTTACTTCGCGCCACGTTACCAATCAAACCCACGACAATGATA  
TCCNNNNNNNNNGTACTAGTCGACGCGTGGCCAAT

## Figure 5-22

**70G12-5 (5X)**

flil gene – flagella synthesis, enzyme: surface structures; flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75008

TANGAAAAACGTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CGCTCCAGCCCCTGGAGAGACGCTTNCCAGTCCGCGCGTTCAAAAATGCCTTGTTGCAAATAGCCCTCCAG  
CTGCGGCCACAGGGCGATGGCTTTATCGAGCATCGGATCGCTGCCTTTGGCATAACGCGCCGACGCTAACCA  
GATCGCGGTTACGCTGAAAACTCGACAACAGCTGTTTGAAGGTGCGCACTCGCGCGTAATGTTGCTCACTG  
ATCAACGCCGTCATTGCGCGGCTGATCGACGCTTCAATATCCNNNNNCNNNGTACTAGTCGACGCGTGGCC  
A

**Figure 5-23**

**71A4-3 (10X)**

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP\_418089

AGCNCGCCGACNTCCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGTCGCTAGTGGAAGCCATTTGAAAAATCCTGGTCATAAAGATGCGATATCCCCCACC GCGT  
ACTAGTCGACGCGTGGCCANANANNNNNNNCGGCANNNCCNCCCNT

**Figure 5-24**

**74B5-2 (2.5X)**

rfaG gene (complement)- enzyme, macromolecule metabolism, LPS; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # S75736

Protein Accession # AAD43826

ATACCCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CGCATTGCATCAACAGTTGCCGCACGGGGCCACCATGTTCCGGGTATATACACAGTCGTGGGAAGG  
CGATTGCCCCGAAAGCATTTGAGCTTATTANGNGCCAGTTAAGTCCCNTACCAACCATGGACGCAA  
TGCAGAATATTATGCCTGGGTACAAAATCATNTNAAACAGCNTCCCNCAAGGATCTGTGTGCGNNGN  
GTTCAATTATTATNCCCTCGNCNGGATTATCTTATTTGCCTGCTNAATGTCNGTCTTCTNATTCCTA  
AATNT

**Figure 5-25**

**76F11-2 (5.5X)**

fliM gene - flagella gene, flagella motor switch biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

NGAAAACGGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
CGCTTGAAGGCTATAGCGACGCTGGAAGGCGATTAAATCCGCTGGAAGTTGAGTACGTGCGTTTCG  
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTTC  
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTTCAGCA

**Figure 5-26**

**77A5-2 (11X)**

b1936 gene - orf; unknown function; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC 000913 (genome)

Protein Accession # E64957

CNCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
ATTACAGGTGCGTAATAAGCTGGTGGCGGCGTATCAGGAAGTGATGAGCATGCAGGTGTAGGTTTT  
GTAACCTGTTGTTAATTACATCCGATCTCACCGCGTGGGGCATGGATGGGGCAAACCTCACTCAATT  
TCTGGTTTAAATGGATACCTGATCCTGAACGTTTTCTGCCATCCACGATCCGTATACGCGATAAC  
CCCCCTGAACATCAGAGCGTCTCA

**Figure 5-27**

**78E3-2 (7X)**

fliA (complement) - flagella biosynthesis, alternative sigma factor

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74989

NAAAACGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GGGTTAATACCAAGTTTTTCGCGCTCCGGCAACGTTTTCGATGGCTTCCATCACCCGCTGGCGCAGAT  
TACTGTCCAGTAGTTGTTGTAGCGGGTTTTCTCGCTGATGATCATCAGTAACCAAGTTTCGATGCTATC  
GCCGTGCTCTTCGCGCCACTCATCGTAGGAGAAGAGCTGGCTGTTATTGGTGTGCGAGCAACATTTG  
GCGATAATCGGCAATATCNCCCCCCCCCGTACTAGTCGACGCGTGGCCAA

## Figure 5-28

### 78F6-3 (2X)

tolA gene - membrane; colicin-related functions; membrane spanning protein required for outer membrane integrity

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000177

Protein Accession # AAC73833

ATACNCGACCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGTTTAGCTGCTGCCAACGCAGCCTGACAAAGTGCGGGATCGCCACCTTCAGGTTTGATATCCAGT  
AACATACCATCGGGTGCCAGTTTTATGCGCAGCGTACAGGTTTTGCCTGCATAGGACGATGCGTCA  
TAGAACTTACTTTTCGATAGCAGATTTAATCTGCCCGGCATAGTTATTGATATCCNCCCCCNNGTA  
CTAGTCGACGCGTGGCCANNTATTCNGATATCNCNCCNGCCNGTCTANTCCNCGTGGNCATATCT  
GATNC

## Figure 5-29

### 85G11-1 (6.5X)

Between 2 promoters (complement) - 1) factor sigma 70; predicted +1 site at 201135 and 2) factor sigma 70; predicted +1 site 2011238

Transposon Tn10 Accession # AY528506

Nucleotide Accession # D89826

Protein Accession # AAC75005

ANNGNAANAGCNCGCCGACATCCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGTCTTGNTCCACTTTGCCAATANCGCCGGCCNTAGCNCTAGNCGNCGCACGNNCAGACGCGTGG  
CCA

## Figure 5-30

### 89A8-3 (6.5X)

fliG gene - flagella structural; flagellar motor component

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75006

CGNTACCGGACCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TGCTCGGCTCCTTTTCAGCGCGATCAACAGCGATTTCGGAATCCACTTCCTGCAACAGACGCTGAATG  
CTGCGATCGTCGACATCCACCAGATTCTCGAACAGGAACATCTCGTCGATGATTTTCTGCGCCAGC  
TCGCCGTCGAATTCACGCACGGCGGTAATAACGGGCTTCTTCTGCTGAGTTTTTC

## Figure 5-31

### 92G7-3 (3.5X)

mhB gene – enzyme; degradation of RNA; product is RNase HII, degrades RNA of DNA-RNA hybrids

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

```
GGAAAAAACGTCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCAGCGCCGCCNTTNN
NGCGTCACGCGTNACTTTTCGCCAGGATAGACGCGGCACTGATTTCCGGTACGCGGCTATCGCCTTT
CACCACAGCCATCGCAGGCATCGGTAATTTTCGGGCAGCGGTTACCATCAATCAACACATATTCCGG
CGCAATATGCAGCCAGCGACGGCAGCTGCATCGCCAGCATGGTCGCATGAAGAATGTTTCAGCT
CGTCGATATCCNNNNNNNCNGTACTAGTCGACGCGTG
```

## Figure 5-32

### 92G9-1 (3.5X)

mhB gene – same clone as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000127

Protein Accession # AAC73294

```
TANGAAAAAACGTTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCNCCNCCNNGTACT
AGTCGACGCGTGGCCAAATATNNNNATATNNNNNNNNNNNNNNCTANNNNNNCNCGNGGNANNN
N
```

## Figure 5-33

### 94G6-3 (4X)

Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # NP\_418089

```
NNNGNAAAGCCCGCGGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAAAGCCATTTTCGAAAAATCCTGGTCATAAAGATGCGATATCCNGNNCCNNG
TACTAGTCGACGCGTGGCCAAANNNCNNNNNNNANNNCNATNCTNGCNCNNCCANC
```

## Figure 5-34

### 98E7-4 (6X)

fliR gene - putative enzyme, surface structures; flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

```
CGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
CACTGAATCTGGCATTAGGTTTACTTAATCGTATGGCCCCGCAATTATCCATTTTTGTTATTGGATTTCCATT
AACTCTGACTGTCGGCATCTCTTAATGGCGGCATTAATGCCGTTAATTGCACCTTTTTGCGAACATTTATTC
AGTGAATTTTTAATTTGCTGGCTGATATTATTAGTGAATTGCCATTAAATAAATCCGTAACGTTTATCATG
TTATCCTAAGGATTATCCGAAAAATAATACCTACGAACATCTTCCAGGATACTCCTGCAGCGAAATATTTGT
TTTAAGCTCACTCACATATCCCNCCCNCNGTACTAGTCGACGCGTGGCCA
```

## Figure 5-35

### 98E11-3 (5X)

flgH gene - structural component, surface structure; flagellar biosynthesis, basal body outer-membrane L (LPS layer) ring protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74163

```
AACNAAACGGNTNCGGCATCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAGC
GCTGCGCATACTTATGCCATATCCNNCNGNNGGTACTAGTCGACGCGTGGCCANATTNNNNNAT
CNNCNNNNNNNGGGGCNNN
```

## Figure 5-36

### 98G12-4 (5X)

mdoG gene - enzyme, osmotic adaptation; periplasmic glucans biosynthesis protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000206

Protein Accession # AAC74132

```
AAACGACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACAAAATCATTAGGGGATTCATCAG
GGGGCAAGTTGCTTTTGGGCGTCTCGTAGCCTTTCCCGGCTAAAGATTGAGCTTGCTTTGCGACAT
CATCAATACTGAAAGCCCAGCTTGAAGATGTATACAGGGTTAACATTACTGCAGCACTCAACCAA
CGCATTTTCATTATTTGTAGCTTATGTTTCATAATTAGTAAGGCACTTCCCCCTTTNGTGTGCTTATA
TCCCTNNGNTNNCNTNCTAGTCNACNCGTGGCCACTNCTATCCNGNNNTCCCCGNTNNGCAGTANT
CAGAC
```



## Figure 5-37

### 103C8-4 (9X)

flpP - flagella biosynthesis, surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

GANNAACGACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GGCTGCGCCCCCTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCAT  
CTACATAAAATTTGTGCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGC  
AATACCTGGTTAGGTGGCGCGGAGGGTGTCCAGCGCGTTACGCAATAAACCAAAAAAATGAT  
GATGCGGGTGAAACTGGTCATCATCAGTAAATTGCCGGAATAAACGTCAACGAGGTGATGAACA  
CCAGCGTCTGCACCGGGAGCGACCAGCTTTGTCCACCGCCAGGCAGCG

## Figure 5-38

### 103E8-4 (7X)

yojN - putative regulator, not classified; product is putative 2 component sensor protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000310

Protein Accession # AAC75276

NATACGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GGTGCAACCTGTATCACACCCGATGAAAGATTAAATAGTCAAGATTATGATATCTTTTAAACGGAT  
AATCCGTCTAATCTTACTGCCTCTGGCTTGCTTTTAAAGCGATGATGAGTCTGGCGTACGGGAAATT  
GGGCCTGGTCAATTGTGCGTCAACTTCAATATGAGCAACGCTATGCAGGAAGCGGTCTTACAATTA  
ATTGAAGTGCAACTGGCGCAGGAAGAGGTGACAGAATCGCCTCTGGGCGGAGATGAAAATGCGC  
AACTCCATGCCAGCGGCTATTATGCGCTCTTTGTAGACACAGTACCGGATGATGTTAAGAGGCTGT  
ATACTGAAGCAGCAACCAGTGACTTTGCTGCGTTA

## Figure 5-39

### 104G4-5 (2.5X)

Between mreB and yhdA genes (complement). mreB: phenotype, cell division; regulator of ftsI, penicillin binding protein 3, septation function. yhdA: orf, function unknown, hypothetical protein, 1232 bp upstream of mreB

Transposon Tn10 Accession # AY528506

Nucleotide accession # M22055

Protein Accession # AAA83892

ANNNCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCANAATCATTAGGGGATTNATCAG  
CTNAATGCATGCNCNACCATTGCCTCNGCTGTTTGCAACCGNGTAAGGNGCATTTCATNTGCATATG  
TTGCTGCNANCAATCTGGCTGAGNAGACAAGCNACTCCCATGANACGCATCGCGCATTATTNTAC  
GTGAAANCGGATNNAANGNTGGNTAAACCNANGANCCNCGCCGANTATNNTCCNCTGNCAN  
NCTNANNTNGNCTNGNACNGANNNCNANNCNACNCCTCTTTNTNNNTTCCGNTNNNGNNGNNNN  
NNNTNGTNTTCCNCCCTGTNTNCANNTNCCNNGNTCNTNCNCCCTCTNTCCANTGCCANTTGTN  
NCNAGGTNCGATNTCTGCNGACCNACNNNTAGNANCCNN

## Figure 5-40

### 107B12-2 (2.5X)

Upstream of promoter - factor sigma 70; predicted +1 site at 3806141

Transposon Tn10 Accession # AY528506

Nucleotide Accession # M80599

Protein Accession # AAC17834

```
GNAANCCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGGATTTTACCAAAATCATTAGGGGATTCATCAG
GCGGTAGCGTGCTTTTTCTGCTTAACCTTAACCAGACAATCACACAAAAGAGTCGCTAGTGGAAAA
GCCATTTGAAAAATCCTGGTCATAAAGATGCGATATCCNNNNNNN
```

## Figure 5-41

### 110E8-3 (6X)

fliP gene – Putative surface structure, flagellar biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
AACGCTNCCGATCCG
GATNATATNAACAGATNTGTATNCACCTTATCTTAATGANATTTTACCANAATCATATTGGGGATATCATAT
ANGGGCTGCCCCCTTTTCCAGCCCCCTACTGCATTGATATTTTNTCTTCGNTGNAT
GGCTGGTACGCATCTACATAANTNTTGACGATCACCGGTGACNTAATAAAANAG
GNCNNANNCANTGCCANTCCCAGCAATNCNTGGTTNNGTGGNGCGGACGGTGCT
NCCATNGCNGACNCACNNAACCNANNNCNATGANGNTNCCNCNGANANTGGA
NATCATCCTGCAANNCNACNGNATNCNNA
```

## Figure 5-42

### 110F12-2 (9X)

Between flhD and insB\_5 genes (complement)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # U88319

Protein Accession # AAC17834, AAC74963

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGATNANCTGCAATAAGCAGAACCNCCTTTTGGNTTAATATGTCCTTACAAATAGAAATGGGTCTTTACAC
TTATCTAAGATTTTCTATATCNCNCNCNNGTACTAGTCGACGCGTGCCATTTATNNNNNATNTCCTN
NTNGTCTCNGNNCNCNCGCGGCCNCANCNNATATNNNTNNNNCNCNTNCACTCTN
```

## Figure 5-43

### 111G8-1 (4X)

flgK gene – structural component, flagella biosynthesis; hook-filament junction protein 1

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000209

Protein Accession # AAC74166

AACCCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GGCTGGGTTGGCAATGGTGTCTACGTTTCTGGTGTGCAGCGTGAGTATGATGCGTTTATTACCAAC  
CAGTTACGTGCGGCGCAGACGCAAAGTAGCGGTCTGACTGCCCGCTATGAGCAGATGTCGAAAAT  
CGACAATATGCTCTCCACCAGTACCTCTTCGCTGGCAACACAGATGCAGGATTTCTTCACCAGCCT  
GCAAACGCTGGTGAGTAACGCGGAAGACCCGCGCAGCGGCCAGGCGCTGATTGGGAAATCAGAA  
GGATTGGTGAATCAGTTTAAACCACCGATCAATATCNCNNNNCCCGTACTAGTCGACGCGTGG  
CCANANNATNCT

## Figure 5-44

### 115A3-5 (2.5X)

fliD gene – flagella biosynthesis, surface structure; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

ATACCNATCCGG  
NTCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GCTTACGCCTGCTTTTTCGTTGTTGATGGCATCACGGATCCCGCTTAACGATGAGTTAGCCGCGCT  
GATATCAATGGTNATCGTACTANTCGACGCGTGGCCATGAATGGTGAGTTTACTGTCGCTGGTGGC  
GATCGCCGTTTTATATCGNCNNTTNCNGTACTAGTCGACGCGTGGCCAAATTNNTNTNANAAAAA  
TTCN

## Figure 5-45

### 115B7-6 (7X)

flgB gene – flagella biosynthesis, cell-proximal portion of basal-body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

AACGGTTACCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CGCGCGATATCGATTTTGCCAGTGAACCTTAAAAAAGTCATGCAACGTGGACGGGATGCAACCAGT  
GTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCGCA  
GAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGACGGTAATACCGTCGATATGGATCGCGAA  
CGCACCCAGTTTGCCGATAACAGCCTGCAATACCAGATGAGCCTTAGCG

## Figure 5-46

### 122F6-1 (4X)

fliL gene - flagella gene; putative surface structure

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75011

```
CGNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACGACGCGTTGCTGCGCTTTGTCGTCAGCGGCAACCTGATGCGAATGCCAGTAGCTGTAACCTGC
GCTGGCACAGGCCGCGAGGGTAATGAATACCAGAATCGGGATCCAAAGCGATCGCTTGCTTTTCTT
GCTTATCGCGTAATCAGTCATGTGTTGCGGTCTTCTGTGTCGCTACTGCTTATC
```

## Figure 5-47

### 123B8-4 (3.5X)

rfaQ gene (complement) – Macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_002695

Protein Accession # NP\_312534

```
AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTAAGTGTGTGAAGCTTTTTTCCAAATACCATGCTGCCGATGACCATAAAGTTGCGATATTTTC
ATCCGTGCAGGTAAACAACGTACCAGCAGCGCCACCATCCACTGATCCGTAAGATTAATGACCAG
GTCATAATTATTCGCACGCAGAGNTTTTATCAACNAAAGCACATTTTAAATTTNATCGAAAGTTCC
CNCNCCTTTATTGCTTANCCCATAGAGCGCANTNNTTCCGGGTTTNCANACAAAATNTGGATGGT
GNCCTGNCNAAGCNCANGTCTANNTNNGCTNTATGAGAATCTG
```

## Figure 5-48

### 123E4-3 (6.5X)

fliR gene – putative enzyme; flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75017

```
AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTACCGTTTTCGGTACGCTGCGTTCGCTCAGAATCGGCGCGGTGGAGATCATCGCCAGCTCN
CGCANTNACGGNCAGAAANTACAGGTTTAAACCAGGATAGCCATTGTTNGCTTGCCACCTGCANCA
AGTACGGTTACCCNATGATTTACTNGNAGGTTAGTGAACAANGTGCGGNCAGTNATTCANCAACA
CATTTNGCATGNTCTGTCTNGGCANNTATTTTGGTGATNAANANGGCCGATNNTTTTNCGANTNNC
CGNNNTGGGNTNCTTNTTCATCNAGTNNCANNATGGGCGNGTATN
```

## Figure 5-49

### 125C9-2 (7X)

fliP gene – Putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000287

Protein Accession # AAC75015

```
TACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCCTTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCATCTACAT
AAATTTTGTTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACCTGGTTA
GGTGGCGCGGAGGGTGTTCAGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGGTGAAACTGG
TCATCATCAGTAAAAATTGCCGGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGCACCGGGAGCGA
CCAGCTTTGTCCACCGCCAGGCAGCGGCTGGCTGGTGATACCCGGCAGTTGCGCGAAGGCGAGGGGCGTAA
TCAGCCAGAGAAGGACAGGTGCGACAGACAATAAACGACGCAT
```

## Figure 5-50

### 125F2-4(3.5X)

rfaQ gene (complement) – enzyme; macromolecule metabolism: LPS core biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_002695

Protein Accession # NP\_312534

```
GNGNAAAAACGTNCCGG
ATCCGGGATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGTGTCTGATAAAGCAGCATATCGATTTTTGCATCANGATAATTCTGCTTGAGCGTACTGAT
GACAGGAGTAGTTAATAACATATCCCCATGATATCNCNNNNCNGTACTAGTCGACGCGTGCC
A
```

## Figure 5-51

### 126G2-2 (7X)

flhA (complement) - flagella biosynthesis; possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCGAACCTGGTATTTTTGCTGTTCACCTGCCGATTGCTCGGGCTGGCCTG
GTGGATACGCGGACGCGAACAAAAAGCGCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAAT
AATACCGTTGTGAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGG
TTAT
GGACTGATCCCGATGGTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTATCCGC
AAG
```

## Figure 5-52

### 126A3-2 (7X)

flhA gene (complement) - flagella biosynthesis, possible export of flagella proteins

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74949

```
ACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTG
GTGGATACGCGGACGCGAACAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAAT
AATACCGTTGTGCAAGCGACGTGGAACGATGTACAACCTGGAAGATTCTCTGGGAATGGAAGTGGG
TTATCGACTGATCCCGATGGTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTAT
CCGCAAGAAATTTGCCAGGAGATGGGATATCN
```

## Figure 5-53

### 132B8-2 (7X)

fliM gene - surface structures/flagellar biosynthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000286

Protein Accession # AAC75012

```
NTNNAAAAACAGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTTGCCCGCCATTTTCGTATGGGGCTGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNCCN
GGNGCGTACTAGTCGACGCGTGGCCAANNNNNNNNCNNCNCNCTAGCNNTAAAAANNNGNCATNANC
CNCNCNCACAANCACNNANGNANNCNTTNCNAAACNANCGTANNATANCCCCNNC
```

## Figure 5-54

### 136E3-1 (7.5X)

arcB gene (complement) - enzyme, Global regulatory functions, aerobic respiration sensor- response protein; protein kinase/phosphatase, sensor for arcA

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000400

Protein Accession # AAC76242

```
NNAAAGCCCGCCGGACATCCCGGATCCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCAAAGCCTGCTTTGANATCCGTAAAGNGCGGACTAANCNACNCGNGGNCNAA
```

## Figure 5-55

### 139G5-3 (5X)

rfaP gene – enzyme; macromolecule metabolism: LPS; phosphorylation of core heptose, attaches phosphate containing substrate to LPS core

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000440

Protein Accession # AAC76654

GNGAAAAAACGNACCGGATCCGG  
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GGTTAAATCCATTAACTCGCGCATCATTTATTATTACCGAAGATCTCACTCCCACAATTAGCCTTGAAGATT  
ATTGTGCCGATTGGGCAGTCAACCCGCTGATATCCNGNCCNNNGTACTAGTCGACGCGTGGCCATANAN  
TNAGCTCNTNCTACNNCCNNANTCCTATCCACCCGTGGCTNCAAGNANCATTTCNGNNNACACCANTTACNN  
NCCAGNCCNCNTCCCCCNNGNCTCNCCTACTCANNACTTCANNANANNATGNCNTTCNNNNGCNNNTCGNT  
CNCCCACNACNNCNTTTTNTTNCNNCCTCTNNCNANCTCNNCCNTNNCNCNTNTNATTCNCCTTTTACCCTNAN

## Figure 5-56

### 152B4-6 (9X)

flgI - flagella biosynthesis, putative surface structure; product is homologue to P-ring of flagella basal body in Salmonella

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74164

GNNGAACGNCGGATCCGG  
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
CACTTTGCATTGATTGCAGTATGGACATCAGATCCATCGGCGTAGCGCCCAGCGCATTGAGCGCGC  
GCACCAAGTTATTGAGGCTGGCGCTGGAACGTACGCTTTGACGCGAACC GCCGCTCTGGCGTAAAT  
CGATCTGCGTTTGTGGAGTAACCAACAGTCTGTCCACCACCAAAACGGTGTATCTGGCTGGCTGACAT  
TGGCCTGACGATTAAGTGTACTGAGAGATTCCCCTGCGCTACCGCGCAGCTGTGAGGGTCACTT  
CGCGATTCATCACCACCGAACC GGTCGCGAGTTAATCACTACTTTAGC

## Figure 5-57

### 163E7-5 (4X)

fliD gene – flagella surface structure; capping protein (same clone as 1B10)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

TNGNAAAAACGTNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTACCGCCGCGCAAAAAGCGACGCTNACCC  
CCATTTCAAATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACGGTACGCTGAAAAGCGCGC  
TGACGACTTTCCAGACCGCCAATACTGCATTGTCTAAAGCCGATCTTTTTCCGCCACCAGCACCA  
CCAGCAGCACCAACCGCGTTCAAGTGCCACCACTGCGGGTAACGCCATCGCCGGGAAATACACCATC  
AGCGTACCCATCTGGCGCAGGCGCAAACCCTGACCACGCGCACCACCAGAGACGATACGAAAAC  
GGCGATCGCCACCAGCGACAGTAAACTCA

## Figure 5-58

### 163F3-5 (8X)

fliD gene – flagella surface structure; Capping protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74991

```
NNANNAACAATACGTCC
CAAGNANANNTGACNAGANGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCNG
GGNCCGGTCTGGATTTAAGTTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGCGACGCTAACC
NCCATTTTCANATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACGGTACGCTGAAAAGCGCG
CTGACGACTTTCCAGACCNCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCANCACC
ACCTGCAGCACCAACNGCGTTTCANTGCCNCCNCTGCGGGNNACNCCATCGCCNGGAAATACCCCAT
TACCGNTCANCCATCTGGCANATGCNGCNAACCCCTTGAACACGC
```

## Figure 5-59

### 167C2-3 (8.5X)

flgB gene – Structural component, flagella biosynthesis ; cell – proximal portion of basal body rod

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000208

Protein Accession # AAC74157

```
AAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCAATCTGCGCGCCCAGCGTCAGGAAGTGCTGGCAGCAAACATCGCCAATGCCGATACCCCT
GGTTATCAGGCGCGGATATCGATTTTGCCAGTGAACCTAAAAAAGTCATGCAACGTGGACGGGA
TGCAACCAAGTGTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGC
CTCCTACCGCAGAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGA
```

## Figure 5-60

### 1G3-6 (16X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_000913

Protein Accession # NP\_415541

```
ATAAAACGGNTACCGATCCGG
GATCATATGACAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATGAG
GGCGCTGTTTCCACAGCCCTTTTAACGTTTCAGGCATTAATATCCAGCACAGTGNCCCTNGNNNNCNCNNN
NNCNTCCACTGATTCAACTGCAGCTTCCAGCTAATATCAATATCTTCGGTGATCATATNAGTCCACNCGGNN
CTAGTCGACGCGTGCCANNANTNNNNCNTTNTTTNTNNCTN
```



## Figure 5-61

### 11E4-3 (12X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA (Not Available)

Protein Accession # NA

```
TTTAAAAACCGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
TGCCAGGCGTCTTTTCCGGCCATTGTCGCAGCACTGTAACGCGTAAAATAGTGCTTTCTCTTACTCTTCTGGC
TGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCNNNNCNNNNGTACTAGTCGACGCGTGGCCA
NANNANTNNTATNTTTNANNACNN
```

## Figure 5-62

### 12F12-6 (23X)

ycdS gene (complement) – putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
TTGAAAACCGCTCCGGATCCNG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTAATTCTGTGGGATA
TCCNNCCNNNCGTACTAGTCGACGCGTGGCCATNTNACNTNCNGCAATNCNTTCTGACACTTCNNNTTNC
TNTNNAT
```

## Figure 5-63

### 14B7-4 (4X)

leuO gene –putative regulator; probable transcriptional activator for leuABCD operon; amino acid biosynthesis:  
Leucine

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
GCNNGCGGTAAACGNCCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGA
GTTAAGCAAACACANCTTNCGNATGGNCGATTTCAACTTATTAACNCGTTTCGATGCCNTGNTGN
AGGAGCCNANCAATTNTTNCAGCCCGCTCATCGCCCTGGGAACCTTCNCCCCCTNCNTTCCTNT
GCTNGCCTTGGGGCCCCCNACNCAACGNAGACNGGGCCNATCCC
```

## Figure 5-64

### 16C8-2 (24X)

Promoter (factor sigma 70, predicted 1+ start site 1986220); upstream of b1904 (orf, unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AACCGTACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTCATCAG
TGCNACGNCNCTNTNANNNNCCATNGATNTNGCACTGTAACGCGCTAAATAACGCTTGTNTCTTACT
CTTCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCNCNCCGTACTAGT
CGACGCGTGNCNATATTATGNNNCCNNNNNCTANTNNNC
```

## Figure 5-65

### 24E12-4 (8.5X)

fucA gene (complement) - enzyme, degradation of molecules: carbon compounds: product is L-fucose-1-phosphate aldolase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC75842

```
CNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTCATCAGAG
GCAAGTGTCAATAATCTGACGAGCAAGTTTATTTTCGTTCCATTAGCTACCTCTCTCTGATTCAAAAC
AGGGCAATAATGTTGTTCCCTTTCACACTATTGAATTAGCCGTTTAATTACCCACCATCTTCTTCCTG
ATTAACAAGAAAGAAATTACACAAGCTTATAT
```

## Figure 5-66

### 26G11-3 (8X)

ycdS gene - (complement), putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000363

Protein Accession # AAC74109

```
AACGNCCGATTCCG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGGATTCATCAG
CCAGATGCGTTCCTGACCCTCAAGTGAGACTTCATGACGCTGGTTACTGTGCGGAAAAATCAGTGAA
AGCCCAGGAGACACCGTACTTACGCCGCTCATTTTATGATACCGGAACATAAGCCTGAGCACTGTT
GCCTGTAACACCATTTTTTCAATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCAGTTGCCAACC
AATACGCCAGTTATCATTAATAATCATACCAGCCAGACAGGCGCGCGCGGGTTTATGCTCATGATT
GAAAACGCGTTCAGCGTACTCTGCCTCGAGCCAGATATTACG
```

## Figure 5-67

### 27F9-2 (2X)

Between promoter (factor sigma 70 predicted 1+ start site 4272977) and yjcC gene (orf; unknown function)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AACGNNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TGCCCAGGGTTTTTCACCTTGCAATGGCCGGGTATAAACAGGCAGGAAATTGANANCANTGAGNCA  
TNNNCNACGANACCAATTNCTGGCNTNGCCGGGCATTATCTTTTAATTCTCTTTCCCATCATTCTT  
TCGCTATGGATTGCCTTCCTTTGGGCAAAATCAGAAGTGAATAATCAGCTCCGAACCTTTGCTCAA  
CTGGCACTGGATAAATCCGAGCTGGTCATT

## Figure 5-68

### 31A4-4 (7X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCT  
TCATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTTCATTATTGACTGTGCT  
TTTTTCGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATT  
TGCCCCGTCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAAC  
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCTGGGTTATCGTGCCACAG  
AATTTCTAATG

## Figure 5-69

### 31G6-3 (2.5X)

Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AAACGACCGGACCG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TGCCNCGCGTNTTTNCCGGCCATTGNCNCAGCACTGNNACGCGTAAAATAGNGCTTTCTCTTACTC  
TTCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCCCCCCCC

## Figure 5-70

### 32A4-2 (14X)

Between ptrB & yebE (complement) - ptrB gene - protease II; yebE gene -unknown function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
NGANNATACGNC CGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GTTGAAACATCTTATAAGGGGTGGCAAAACTCACCGGGGATGCAAGCGAAACAGGGGAGTCATTG
CTTAGATGATGACAGGTAATGGCGCGGATATCGAATGTTATGCAANCAGANAANANCAGNCTGTT
CAAATGGCTGTGCGATTCTGGATAGCCCCGAAATAGTCAACTTCAGGCTATCCAGAGAGCGGAATT
ATTCCGCCAAAGTGC GTTTTTGCTGTTTCGAGATCGCGTTCAATGCCGTCACGAACATCCTGGGGGA
TTTTCAGCGCGTCACCCAGTGCATTAGGTAAGTGC GTTCCATAAAATGGTCAATATCAATAGCCG
CGNNACTAATNNACNCGNGGCCNAGCGCCTCTTC
```

## Figure 5-71

### 35C6-2 (6.5X)

hscA gene (complement)- factor, chaperone; product is heat shock protein chaperone, member Hsp70 protein family

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000339

Protein Accession # AAC75579

```
CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGACGGTCTTTTGAGCGTGACGGCGATGGAGAAATCCACCGGCGTTGAGGCGTCTATTAGGT
CAAACCGTCTTACGGTCTGACCGATAGCGAAATCGCTTCGATGATCAAAGACTCAATGAGCTATGC
CGAGCAGGACGTAAAAGCCCGAATGCTGGCAGAACAAAAAGTAGAAGCGGCGCGTGTGCTGGAA
AGTCTGCACGGCGCGCTGGCTGCTGATGCCGCGCTGTAAAGCGCCGCAGAACGTCAGGTCATTGAC
GATGCTGCCGCTCACCTGAGTGAAGTGGCGCANGGCGATGATGTTGACGCCATCGAACAAGCGAT
TAAAAACGTAGACAAACAAACCCAGGATATCNCCCNNNCNGTACTAGTCGACGCGTGG
```

## Figure 5-72

### 37B5-2 (11X)

yedK gene - hypothetical protein, function unknown

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000285

Protein Accession # AAC74998

```
NGAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
CTCCGCGCCCTGGTTTTTAACATTACCCACCGCGCGCGATATCNNNNNNNNNNGTACTAGTCGACG
CGTGGGCCAANTANNNNNNCNNNNNTNNNNNNNNTNNNNNNCGNNTNNNGNNNNNNCNC
```

## Figure 5-73

### **41G10-2** (10X)

leuO gene - putative reg of AA biosynthesis (leucine) - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAAGCAAACACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCCNNCNGTACTAGTCGACGCN
GN
```

## Figure 5-74

### **41B10-5** (9X)

leuO gene - same as as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAAGCAAACACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCC
```

## Figure 5-75

### **44C2-1** (10X)

ycdS gene (complement) - same clone as 31A4-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCT
TCATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAAGAGCTCGGTCAATTATTGACTGTGCT
TTTTTCGGCTGATGATCTTTTGAGATAAGCCGATGCAACCCAATATTGCCCCAGGGCGGAATAATT
TGCCCGTCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAAC
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCT
```

## Figure 5-76

### 46E5-5 (10X)

ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

AAAAACCGTTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GAGCTGGNGCGTTTTCTCCCCACGGCCAGTGGCGTTCACNATAGACCCAGAAATAGACGCCGNCNACAATN  
CACATAATGGACATAAAAAACGGCCAGAAGAAAACGAACCTNATCATCAGTTCACCGAGTGAAAGTACGC  
TACGCATAGGGGTATGCATAACACCAGACATAATATAAAAAACGATACGATGCGATTAA

## Figure 5-77

### 48A4-5 (20X)

trs5\_11 (complement) - IS, phage, Tn; transposon related functions, IS5 transposase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000427

Protein Accession # AAC76530

GAGATACGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
TGCTCCACCCTGGCCCGGATGCTGGCTTTTATGTATTTCGATGTTGATGGCCGTTTTGTTCTTTCGCTG  
GATGCTGTTTCAAGGTTCTTACCTTGCCGGGGCGCTCGGCGATCAGCCAGTCCACATCCACCTCGG  
CCAGCTCCTCGCGCTGTGGCGCCCCCTTGGTAGCCGGCATCGGCTGAGACAAATTGCTCCTCTCCAT  
GCAGCAGATTACCCAGCTGATTGAGGTCATGCTCGTTGGCCGCGGTGGTGACCAGGCTGTGGGTCA  
GGCCACTCTTGGCATCGACACCAATGTGGGCCTTCATGCCAAAGTG

## Figure 5-78

### 49C2-1 (9X)

ycdS gene - (complement), putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG  
GATGAATTACGGGCGATGACAGAGTCATTACCTGAAAATGCATCTACGCAACAATATCCACNNA  
NTNGTACTAGNCGACGCGTGGCCATCAACTTGCTGCCGCGATTGACGATGCCAATTTAACGCCAGA  
TATTCGCGCTGATATTNCTANNCGACGNGCNGGNGACGCGTGGCCAANGCNNNNCNTNNCTNN  
NAANNNTGNNGCNGNCTGGCTGNTGTCCNNCTGNNANCGCCNCANAACNTCNTGNCNTNNN  
NNANGCTGNCGTCCCTTANNGAAGNGGCCNNGGNNNAATNATGTNNACNCCNTNNCCAANCNTTN  
NNNACTNNACNANCNACCCNNGATNTC

## Figure 5-79

### 49G12-3 (20X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CACGGATCCGG  
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CGTTAAATTGGCATCGTCAATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTATTCTGT  
GGGATATCCNNCCCNCCCGTACTAGTCGACGCGTGGCCATGNNATNNNCCGNNATTCATNCTGAT  
GACNCCCGCNCAGTTTATANATATNNNNNNNNNNGTNCT

## Figure 5-80

### 51A10-4 (2X)

modC gene – ATP-binding component of molybdate transport; Transport of small molecules: Anions

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGCACCGGATCCGG  
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
ACTGACGCGCCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAAAGGTATC  
TGCCTTNCCGTAAGTCGACGCGTGGCCACNNNTTCATTNCNCTANCTCNNAAGTNNNCCNACTCCGN  
GNNCNAACNNCCNNNCCCNCTNGCAGNCNTGTNCNCNNACNNCGGCNACCCNNNGANNNGNCTCCNCCC  
GCCCCCTNTCNNACCTNNNNANGGCNTACCNCCCCCTCNGGCTCNGTTACCTTNNNTNNCCGNCCCCN  
CTCANANNCCNCTNACNNGNCNNNCNATNCNTCGCNNNNNNAGTANNCCCNCTCCCCCACNCNCNN  
CCGTNTTNNCCTTNAGANCT

## Figure 5-81

### 56C11-1 (5.5X)

modC gene – Same clone as 51A1-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73852

AACGNACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
ACTGACGCGCCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAAANGGTNTC  
TTGCCTGNCCCGTACTANTCGACGCGTGGCCAAACNAACCTNCTTCNTANNNTCGCANNNTCCCCCTTCNGCNC  
NTCANNCACTCCCNCTGCTCCTNCNNCTTCCNCGCNCNCTACCNCTCGTNNCCTTANTCCACCTGCNNCTA  
TCCCNCGGCCCCGNCTCCCGNCCCCCNCTNCAANTNGTTCAANGNACNGNCCNCCCTCGCCCNAGCGCTNC  
CNGNGCCAGNNCTNTTCATNTCCCTCCCGATCCANTCNCNNCCNTTNCNCTCTNACNNNCCNGTCNCTN  
NCCCCCTNNTTAN

## Figure 5-82

### **62C9-2** (20X)

yecK gene (complement) - putative enzyme (cytochrome C type); not classified ,product homologous to TorC cytochrome of TorCAD resp. system

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000281

Protein Accession # AAC74943

```
CNCGACCGG
GATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTTCGCTGTCTTTTGTGCTTTGTTATGCATTTTCTGCGCAGATTCACTTTGCGAGGCAATATCC
ATGGCATCAAAANAATGGCAACTACGGCACGTTGCAGAGTCAGTGGCTTTTAATTCTTTCCATACT
GTTTCGGCCATTTTCCTGGCGATGAGCTTCGAACCTATCGTCACTGTCTATTTTGCCGCTAACAAATT
CATGATAAATATCTTTAGATGC
```

## Figure 5-83

### **63E2-3** (2X)

between genes clpP and clpX -- clpP: enzyme; degradation of proteins; ATP-depquent proteolytic subunit of clpA-clpP serine protease, heat shock protein F21.5. clpX: enzyme; degradation of proteins, ATP-dependent component of serine protease, chaperone.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
AAACNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
GGTTTTGACCCATGACAGATAAACGCAAAGATGGCTCATGCANATTGCTGTATTGCTCTTTTTGCGGCAAAA
GCCNNCATGAAGTGCGCCAGCTGANNAGCCGNGCCATCCCTNTATATCNCCNNCCCTGTACCTNGNCGGN
CNCGTGGNCNNNCTCCTNTCNTTNNCNTCTCCCNNTCTNNNNCCCCTCTNCGCGGNGCCNCTGANNCGC
CTCNCTTCTTNTACCTCCNCGNGCCTCTACCNCTCGNNCCTCNCCCCCACCTCCTTATTCNCCTCCNTCNT
NTCCNTCTCCACCTNTCCTTTCCNACCGCNCNATNNNACGTCTCNTTCCCTNNNNCCACNNNTNATCCTCN
GCNCCCCTCNGNGCGAANCNTCNCTNNNCTANCGGCNCGNTGNNCNTGCNNCNCANTNANCNCNCNTNA
TTGAGTGCGNGT
```

## Figure 5-84

### **66E10-1** (12X)

ycdS gene (complement) - putative outer membrane protein, same as above

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
CNCGATCCGG
GATATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACGACATCCGTGCCATAATGTTTTTGCCAGGAGGCACCAACACCTGCGCTGAATATTTGCTCCCAGCTA
TTTTCATAGCTTCGCCATAACAAATGGCTTGCTCAAATGCCGGAACAATATCNNNCNNNNNGTACTAGT
CGACGCGTGCCA
```



## Figure 5-85

### 68E11-2 (2.5X)

glnE gene (complement) – enzymes, translation and modification; Adenylylating enzyme for glutamine synthetase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000387

Protein Accession # AAC76089

AAACCCACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGTTTTATCTGCGTCTGGCGCAACGCATTATGCATCTGTTTCAGTACGCGTACCTCTTCCGGCATT  
GTATGAAGTGGATGCTCGACTGCGTCCGTCGCGGGGCGGGGAATGCTGGTGACATCCGCAGAAG  
CATTTGCCGATTATCAGAAAAACGAGGCCTGGACGTGGGAACATCAGGCGCTGGTGCGTGCGCGT  
GTAGTGACGGCGATCCGCAGCTCACCGCGCACTTTGACGCAGTGGTTCGCGAGATTATGACGCTG  
CCGCGTGAAGGTAAAACCTCTGCAACCGGAAGTGCGGGAAATGCGCGAGAAAATGCGCGCTCATCT  
CGGCAATAAACATCGCGATCGCTTTGATATCAAAGCTGATGAAGGGGGAATTACCGATATCGAAT  
TTATTACCCAAT

## Figure 5-86

### 68A3-1 (>24X)

wcaI gene (complement) - putative enzyme, colanic acid biosynthesis

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_000913

Protein Accession # NP\_416554

GNCNNCTAAAAACNTTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN  
GGCCGNANNGGTGTGGCGCTGCCCGCTGTATGTGCCAAAACAGCCGAGCACCTGAAACGCCTGT  
TGCATCTGGGCAGTTTTGCCGTCAGCAGTTTCTTCCGCTGATGGCGCAACGTCGCTGGAAGCCGG  
ATCGCATTATTGGCGTGGTGCCAAACGCTGTTTTGCGCGCCGGGAATGCGCCTGCTGGCGAAACTCT  
CTGGTGCGCGTACCGTGCTGCATATTACGATTACGAAAGTGGACGCCATGCTGGGGCTGGGCCTTG  
CCGAAAAGGCAAAGGCGGCAAAGTGGCACAGCTGGCAACGG

## Figure 5-87

### 73E6-6 (16X)

ycdS gene (complement) – putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

CGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CGCATCTGGTCTTACCATATTTGATTGTGCTGATTTCTACCCAGTCTGTATTACGAACAAAATACAG  
AACACGATACCCATACTACAACCTATAAAAACGTTTCGATATNGTTCCGGCCTGTGCTGCNCGNC  
NNGTGGNCTGGCGAAGCTATGAAAATAGCTGGGAGCAAAATATTCAGCGCAGGTGTTGGTGCCTCC  
TGGCNAACCAATTATGGCACGGATGTCGTACCCAACTCGGCTACGGGCAACGCATTAGTTGGAA  
TGACGTGATTGATGCTGGCGCAACGCTACGCTGGGAAAAACGACCTTATGACGGTGACAGAGAAC  
ACAACTTATACGTTGAATTCGATATGACATTCAGATTTTAAAGGATAAATATGTTACGTAATGGAA  
TAAATA

## Figure 5-88

### 73E9-1 (12X)

ycdS gene (complement) - putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

ACGNCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAATCATTAGGGGATTCATCAG  
CACCGTACTTACGCCGCTCATTTTGTATACCANCGAACATAAGCCTGAGCACTGTTGCCTGTAACACCATTTT  
TCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCAGTTGCGAACCAATACGCCAGTTATCATTAATA  
TCATATCNGCCNGNCCNGTACTAGTCGACGCGTGGCCANAAATTGAAAACCTGGTTTGCANAAATTNTCTNG  
ATCNCCTAAAAAGCTATNACTGGACNCGNTATNATGGNTNTGNNTTATCTGGNANGGGGNNNCANAAAAA  
TNCGNTGCCAATGGNTNATNCAATTGNCCATNAAATTAACATCCCTTANGNTNAAAGACAAATNNATT  
TTNTAATTCANGGGCNA

## Figure 5-89

### 73F2-1 (12X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NNGNAAACCAGCCGGACNTCCCGGATCCGG  
GATCATATGACNAGATGTGTATCCACCTTAACCTAATGATTTTACCAAATCATTANGGGATTCATCAG  
NCAGATGCGTTTCCTGACCCTCAAGNGAGACTTCATGACGCTGGTTACTGTTCGGAAAAATCAGTGA  
AAGCCCAGGANACACCGTACTTACGCCGCTCATTTTGTATACAGCGAACATAAGCCTGAGCACTGT  
TGCCTGTAACACCATTTTTTTCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAAC  
CAATACGCCAGNTATCATTAATAATCATATCNCNCCNGAAGAGGACTAGTCNACGCGTGGCCANNAC  
ANCCNCACTNNNTAACNTGNGGCTACNANTNTACCNGCCCANNAGNNTTACNTNANTTNCGCNCN  
CCTNCCANTCNCNCCCNANGTNNNCNNAANCTNNANNCTN

## Figure 5-90

### 75E11-5 (1.5X)

moaC gene - enzyme, biosynthesis of cofactors, carriers: molybdopterin; molybdopterin biosynthesis, protein C

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000181

Protein Accession # AAC73870

NNAANATACGGTTCGGGNTCCG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAATCATTAGGGGATTCATCAG  
ATGGAAGCATTAACCGCGGCTCCGTGGCGGCGCTGACCATTATGACATGTGCAAAGCGGTGCA  
AAAAGATATCNCNNCCNNNGTACTAGTCGACGCGTGGCCAAANATCNGGGNTCTCNNNNTGCTN  
GCTNCNAATCNANTGNACCCNCTNAACCCNTTCNAGCTAAACATNTNNATNTGNAACNNATAAAC  
NCAGGACGNCATATNGGTNNACNT

## Figure 5-91

### 84A10-6 (11X)

ycdR gene - orf, unknown function, product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

```
CGNNGANACGNCCGAATCCG
GATANTANACAAGATGTGTATCCCCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCCGCTT
TAAAAGTCGTGCGTTAACTGACTTCACCTTAGAACTTAGTGCGCGCTAAAAGCCATTCGCGGTCC
ACATATTAAAACGACGAAATATTTTGCACCTCCGGTAATACAACCTGAAAGTGAAGCCTGGTT
TGCACAGAATTATGCTGATTTTCCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCT
GGAAGGTGTGCGAGAAAATCGGCTGACCAATGGTTAATACAATTGA
```

## Figure 5-92

### 86E7-6 (10X)

ycdQ gene (complement) - orf, unknown, putative enzyme homologous to IcaA in *Staph*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
NACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCG
ATGTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTG
GTGGGTAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATC
TATGGAAACGTATTTACCGTTT
```

## Figure 5-93

### 86F11-6 (11X)

ycdQ gene (complement) - same clone as 86E7-6

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

```
NCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACCTTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCG
ATGTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTG
GTGGGTAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATC
TATGGAAACGTATTTACCGTTTCC
```



## Figure 5-97

### 90E7-1 (2X)

aroD gene – amino acid biosynthesis, Chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000264

Protein Accession # AAC74763

ACGACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TGCTCGCCGCCTTCTTTGGCACTGCGGAAGGTAAACAGCAGCNGTTTTCTGGCATGGACTCACGGAGAATT  
TTTGCTGCCGCCATGACAGACTCCACATTGGAGNGGTANGCATNCTGGNCCACACNCCATTCCANANTATC  
NNCTTTNNCTGCNACTANTNANNNCTCGNANTNTTNCNTCNCNNNNCNCNCANTTCCTCNNCCTTNNACNN  
NCGNGNNNNTTGTTGAANNNTTNNACANCNCANNTTCNCCCCNCNTCTNNTANATNNGNCCCNGCCTN  
NNAGTNTANTNCNNTTTNNTC

## Figure 5-98

### 91F9-6 (2X)

b2531 gene – orf, function unknown; hypothetical protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_000913

Protein Accession # NP\_417026

CGTACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN  
GGGCCCCGGTACCGTTGGCTGATATTTCCGAACGTCAGGGAATTTCCCTTTCTTATCTGGAACAACTGTTTTT  
CCGTCTGCGTAAAAATGGTCTGGTTTCCAGCGTACGTGGACCAGGCGGTGGTTATCTGTTAGGCAAAGATG  
CCAGCAGCATCGCCGTTGGCGAAGTAATTAGCGCCGTTGACGAATCTGTAGATGCCACCCGTTGTACGGGT  
AAAGGCGGCTGCCAGGGCGGCGATAAATGCCTGACCCACGCGCTGTGGCGTGATTTGAGCGACCGTCTCAC  
CGTTTTTCTCAACAACATTACTT

## Figure 5-99

### 93E3-6 (12X)

ycdR gene (complement)– orf, function unknown; product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCGCTT  
TAAAAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTTCGCGGTCC  
ACATATTTAAACTGCACGAAATATTTTGCACCTCCGGTAATACAACCTGAAAGTGAAGCCTGGTT  
TGACACAGAATTATGCTGATTTTCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCT  
GGAAGGTGTGCGAGAAAAATCGGCTGACCAATGGTTAATACAATTGACCAATCAAATTAATAAACA  
TCCCTCAGGCTAAAGACAAATCTATTTTAGAATTACAGGC

## Figure 5-100

### 96B10-1 (11X)

nhaR - regulator, transport of sm molecules - cations; encodes a positive regulator for nhaA( a Na/H antiporter)  
stimulates transcription of osm-c

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000112

Protein Accession # AAC73131

```
NCAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
GTTTATGCTGACTTAATTGCTCCAGCAGCATTTTCGTGGGTGGATTTCGAAGCAGCGAAGATGAATGG
GCTCGCCTTCTACCACTGCGGCGTTAAGTACGCTACTGACCAGGCGTTTGGAAAGTGCATCAGCCA
CGCCAAACGTCAAACAATAAATTGGATTCTTTGCGATAGTTCACAATATCCNNCNNNNCCGTACTAG
TCGACGCGTGGCCAN
```

## Figure 5-101

### 102G9-5 (5X)

leuO gene - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAACNCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAAGTGGAGTTAAGTATGCCANAGGTACAAACAGATCATNCAGAGACGGNNGG
AGTTAAGCAAACACAGCTACAGCATGGTTCGATCTCAACTTATTAACCGTTTTTCGATGCCGTGATG
CAGGANCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCNNNNNGCNGNACTAGTTCCG
ACGCGTGGCCNCATANNATGTNTCNNNTTCNNNNCTCTTCNNTTGCTTCCCTTNCCCCCTCTTCNNGC
CCCCANNNCGTCTNNTNTNATCNGNNGNCTTNNCNTACGACTN
```

## Figure 5-102

### 106B2-6 (5X)

leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

```
AAACCCNTNGGATCCNG
CATCATATGACAAGANGTTGTATCCACCTTAACCTAATGATTNTTACCAAAATCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGTGGAGTTAAG
CAAACACAGCTACNGCATGGTTCGATCTCAACTTNTTAACCGTTNTCGATGCCGTGATGCAGGAGCAAAAC
ATTACTNCGTGCCGNTCATGTTCTGGGAATATCCCNNGGNNACGTNCTAGTCNANGCGTGGCCAANNNGTN
NGGNNNCTNANTCACAGNANCTTTANNNGTN
```

## Figure 5-103

### 109B4-4 (2X)

Between two protein binding sites (complement) - 1)central position to predicted promoter: -0.5/LexA predicted site and 2)documented IrP site/ central position to leuABCD promoter:- 156.5

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

AGCNCGCCGGACNTCCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TCGGTAGTTAAGCAGAAATTAATATCGCTTACTTTAACCACCGCAGCACAATTAGCTAATTTTACG  
GATGCAGAACTCACGCTGGCGGGACGTTTTTATTGCGTCAGGGTTGACATCCGTTTTTGTATCCAG  
TAACTCTAAAAGCATATCGCCCCNCCNGTACTAGTCGACGCGTGGCCANAACNCGNNNTCCAN  
TNTNNCC

## Figure 5-104

### 110G8-2 (9X)

ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

GNAANGNAAAACNCGCCGGACATCCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
NACNGCNNATTGNNCCACGGNNGGANTAANTNGCCCCNGNTTGNNTCTCGCTGNTAANGANAAA  
TAACGTCTTTATAACGANCGCGAGTNAATAACGCGCCAAGATGATCAACCTGAATACNCTGGTAC  
TGGGCAGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCG  
ATCGGCAATGGCATAACGNTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGC  
ATGAATATCAGNNNTTGNNTGNACTAGNCNACGCGTGGNCAAAACAT

## Figure 5-105

### 115C12-5 (16X)

ycdR gene (complement) – orf unknown function; product homologous to lcaB in S. aureus

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

CGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGCTTAATACCGGCATCCACGCATAGATGTTTACACCTGAGCGGGTACGTAATTGCCAGGCAACCC  
GACTAAAAATATCTGCTTTCATTGGNCTNANACAANCNGGANCAGACCTCTTTGACCAGCCCAT  
CACCATCGGGGATCAGCAAATGCCTGCAAATACACGGTTGATATTTGCATATCTTTCCCCNCGTAC  
TAGTCGACGCGTGGCCACATTACTTNTANTNTANNANTGGATCCNANTNANNCGGNTNTANCTNG  
CCTTGNANGGGNGNANNATTATCNNCTGCCNNGACNAANT

## Figure 5-106

### 123F5-6 (4X)

modA gene - transport, small molecules: anions; molybdate-binding periplasmic protein; permease

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000179

Protein Accession # AAC73850

```
TTTNNGAAACACGCCGNACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAAATCATTAGGGGATTCATCAG
TGGATTATGCGGTTGATAAAAAGCGATCGATACAGCTACGCGTCAGACACTGCTCGGCAATAGC
CTGGTCGTTGTAGCACCAGAAAGCCAGCGTGCAGAAAGATTTCACCATCGACAGCAAAACCAACTG
GACTTCACTGCTGAATGGCGGTTCGCTGGCGGTTGGCGATCCGGAACATGTTCCCGCTGGCATTTA
TGCAAAAGAAGCACTGCNAAAACCTGGGCGCATGGGATACNCTCNCTCCGAAAATGGNCCNCNTA
AGNTGNTCCTAGGGGNNCNCNNCGCNGGTCAACACNTAATCGAACCN
```

## Figure 5-107

### 125A7-1 (2.5X)

rbkK gene - enzyme, degradation of small molecules: carbon compounds; ribokinase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000452

Protein Accession # AAC76775

```
GCAAAAACGANNCGGCCAAG
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAAATCATTAGGGGATTCATCAG
GAAAGGGCAGCNTTANCGCCGGCATGAATACCGATGACATTCTCACCTTCGCCATTAAACAAAAAT
CANCGCCACACCTGTTGATTTCGCTTTGATCTCGCTGACCGGAGTAANATCCCCNTNNNNGNACTA
GTCNACGCGTGGCCATNAANTTCNNNCGACNTANGACCCNANTCCTGNNNTTAANNCCNCGNNTN
CCNTANTTGCNCCANNNN
```

## Figure 5-108

### 125E4-1 (24X)

insB\_4/insA\_3/insA\_2 genes (complement) - all three have the same probability score and identities,89% - IS,phage,Tn; transposon-related function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NA

Protein Accession # NA

```
CACANCCGNACATCNGCGNT
ATNNCTACTNANAATGNCGTGAANTATTNCNACTGCNTNACACTTACACCGNNTTCATNCCGGTANGC
ACCACANAAAANNITGAATATGAGGCATGAATGGTNGTTGGANGCCGGGTAAACAGCCNTCATTATG
GGNGTTGGCCTCAACACGATTTTCCTCCNTTTAAAAAACTCACGCCGNTACCCTGTAACCTCGCAC
CATACTGGCAGGGCAGCNGACNGATTTCGCTGCGCATGAAATGNANAAACNNTGGGGATNCACCA
GGNGTAAATCTNGCCAGCGATNNCTGNNTTNNCTTNTGANANGATNCNGAAAANGGGGGNTGC
NCNCGTNTNCCGGNAAACATCNNTAATAAACTGGGGCCAAAGTAAAACGTCNGGATATCCAATC
CANNGTACTANTCGACGCGTGGCCANNACTGNC
```



## Figure 5-109

### 126C5-4 (7.5X)

leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

NNACGCTNCGGNNCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN  
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG  
TTAAGCAAACACAGTCTACGCATGGTCGATCTCAACTATTAACCGTTTTTCGATGCCGTGATGCAG  
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCCCNCNTNNGTACTAGTCGACGCG  
TGGCCANN

## Figure 5-110

### 130E8-4 (24X)

Between yecK and cutC genes (complement) - in a protein binding area with no predicted promoter; TyrR predicted site

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000118

Protein Accession # AAC73187

ATNCNCGACCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN  
NGTCCAGTAATTCAATTANAGGAATCTATGCGNGGGANAAACGGNTGGCNGCTNCNCGCTAANGC  
NAANAANTAANCCNCCTNNNNCTANGTATNNNNGGNCNNTNNNANNNCNGNTTTCT

## Figure 5-111

### 130G11(2.5X)

aroD gene - enzyme: amino acid biosynthesis: chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000264

Protein Accession # AAC74763

ANNCNCGACCGG  
GNTCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TCNGGCCGANCNGGCNATTTCCACCGAGGCTTATNTCCNCNNNTNTCGNNCTAGNCGNNGCNTGG  
CCANGNTTNCNCCNCCNNTNACNCNCTCCATNANTNTNNCCNCTNTCNCNNANTACNGTGCCCGN  
GNATNCCCNTCCTCCGTCCGCCCCCNCNNGCTTAGCNGCNNANTGGCCNNNNNNCAANTTANGAC  
GATCNGCCNGCCCNNTNAAACNGNGTTNGCCATNTNCNTNCNCTNTTATN

## Figure 5-112

### 140B5-1 (9X)

miaA gene – enzyme, Aminoacyl tRNA synthetases, tRNA modification; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000489

Protein Accession # AAC77128

CGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
AGGCAAGTCCGTATGCAAATCTCCTCGGGCAAAAAGCGCCCGGACTTCTGCTTCAAAACCTGAAG  
CCAAACATCTGATGAAAACGCTGCTCAATGCGTTGATGGAGCAGTTCACGGCTCGCCGGGGCGATG  
GCGAACTGATGCACCTGATACGGTAGAGCGTCTCCTGACGTTTGCCTCAGTTCCGTTAAAGTTTTA  
CCCGAAATGAAAAAACTTCCAGTGCCCGGGAAAGCCTTTGTGGATCATTTGGATGAATCCTTGCT  
GCCGCAACCGGATCTACCTCCTGAAGTTGACGATGCAATGACTCCCAACCTTGCTCTGCCGCCTGT  
TGCTCAATTCTGGCCCGTACTTCCGGGTCTGCCGACGGTAGCGGCGACAACCCTTCCAGCAATGCC  
TTGAAAT

## Figure 5-113

### 141G2-2 (16X)

yjjQ gene - putative regulator, not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

GNCGGATCCGG  
TATATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GATGGGGCATCAACCAGATAGCTTCATTGCTTAAAGAAAAGTAATAAACTATCANCGCCCAAAAA  
AACAGTGCATGCGTCCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGC  
GCAGGGTGCAAGAGAACTTAACCTTGCCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCG  
AATTAAGAAGAGAAATGTGCGCACTC

## Figure 5-114

### 141G4-6 (18X)

ycdS gene (complement) - putative outer membrane protein; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74109

NNNAAAGCACGCCGGACATCCGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
ACCCAATATTGCCCCAGGGCGGAATAATTTGCCCGCTCTTTTTAATCGCTGATAGTGAGAAATA  
ACGTCTTTATAACGATCGCGAGTTATAACGCGCCAAGATGATCAACCTGAATACGCTGGTACTGGG  
CAGTCCGGTCTGGGTTATCGTGCCACGAAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCCG  
CAATGGCATAACGTTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGCATGAA  
TATCANCGCGAATAGTACTAGTTCGAC

## Figure 5-115

### 145F10 (3X)

ykgK gene (complement) - putative regulator; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000136

Protein Accession # AAC73397

NNNNGAAGCNCGCCGACATCCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG  
TACCACGCCCTAATATTGCTATTGTAATACCAATAATTTGCTAAGGCCTCTGACTTTCTGGCCGCA  
ATCAATACGACCTGTTTCCCCTTTACCGCGGATAACCATTCAATTATCACGGTTTATAAATTCAGATA  
AAGAATCCGTACTGAGATTGATAAACACGAAATCTTTTCTAATTTTCTCCAACGATAGATAAATTA  
ATCTGTGCGATATCCCCNNCANNNGTACTAGTCGACGCGTGCCCA

## Figure 5-116

### 150E3-6 (20X)

ycdP gene (complement) – orf, hypothetical protein unknown function

Transposon Tn10 Accession # AY528506

Nucleotide Accession # NC\_000913

Protein Accession # NP\_415540

NACGACCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTAGGGGATTCATCAG  
GGCCAGAAGCCGACTTCAGTTCTATTTTTGCTGGCAGTGGCGAATGCCGTCGTGTTAATTGTCTGGGCGCT  
GTACAATAAGCTGCGTTTTCAAAAACAGCAGCATCATGCAGCCTACCAATATACGCCGCAAGAATATGCAG  
AGAGCTTAGCAATACCTGATGAGCTCTATCAGCAACTACAAAAAGCCACAGGATGAGCGTACACTTCACC  
AGCCAGGGGCAAATAAAAAATGGTTGTTTCAGAAAAAGCGCTAGTCCGGGCATAAACACCCAAAAACAAAGC  
CCGGTTCGCCCCGGGCTCTGCACCGATAACACACTTAAGTGTAGGCATGCAGCGTACGTTGGCAAAGTGCCG  
AACGTACGCANT

## Figure 5-117

### 150G7-2 (4X)

prfC gene- Factor; protein translation and modification; peptide chain release factor RF-3.

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000508

Protein Accession # AAC77328

ANACNCGTCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAATCATTANGGGATTCATCAG  
TGTGGTGTCCGGTAAATATGAAAAAGGCATNAACTGCNCCACGAGCCCACTGCNAANGATGNNG  
NAATCTCCGCCCGCGCCTCTCTGGCNGGTNNCCGTTCTCACCTNNACACNCCCCNNGCTCNC  
NTNCNCTCCCNACNNCNNNTTCTCTCNGCANCCCACTTATCTNCCNNCNCCCTCCCNACGNNTC  
CCNCCCCNCGNNCNANTGNNTTGGCTNCCGNCNNNANNNCNCTCNTCCTGGCCTCNCNTT  
ACNCCN

## Figure 5-118

### 155F4-4 (20X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

NNCGATCCGG  
GATCATTGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
CACTTGTTGCCACGTGGCAAATATTCTCGATCGACCAACTCATCGCCAAATTTTACTTGTTTATCC  
GCTGGCATATCNNCCNNNNCGTACTAGTCGACGCGTGGCCANN

## Figure 5-119

### 160A8-6 (20X)

yjjQ gene – putative regulator; not classified

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000507

Protein Accession # AAC77321

CGNCCGGATCCGG  
GATCATATGACAAGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
GGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAACTATCAGCGCCCAAAAAACAG  
TGCGATGCGTTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAGG  
GTGCAAGAGAACTTAACCTTGCTTCTGTTTATGGAGATGCCGAGAATGGAACACAGCCGAATTA  
AGAAGAGAAATGTCGCACTCATAGAAAAATGCGTCATGAGTAGTATCGGTATTGAGAGTTTATTC  
AGAAAGTTTGCGGGTAACCCTTATAAGCTCCATACCTATACCAGTCAGGAGTCATTCAGGATGCC  
ATGTCGCGGATATCCCNCCNCCNCGTACTAGTCGACGCGTGGCCAA

## Figure 5-120

### 169G4-6 (18X)

ycdR gene (complement) - orf, unknown, product homologous to IcaB in *S. aureus*

Transposon Tn10 Accession # AY528506

Nucleotide Accession # AE000204

Protein Accession # AAC74108

AAAANCNCGCCGGACATCCCGGATCCGGGATCAT  
ATGACAAGGATGTGTATCCACCTTAACCTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG  
TATTAATCGCCAATAATCCCTCATTAAGAGAGTTTGCCCAAGCAAAATTATTACCGTACAGGAAAAAT  
CACCACAACGGATAATGCATATCNCNCCNNNNNGTACTAGTCGACGCGTGGCCACANAN